

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### seq id no:3 vs. McCaffrey no.1

Results for: **lcl|55517 None(206bp)**

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|55517

lcl|55517

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

206

#### Subject ID

55519

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 3582

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

**[?]**

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

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Blast 2 sequences

### seq id no:3 vs. McCaffrey no.2

Results for: **"lcl|28559 None(206bp)"**

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|28559

lcl|28559

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

206

#### Subject ID

28561

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 3582

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

**BLAST Basic Local Alignment Search Tool**

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Blast 2 sequences

**seq id no:3 vs. McCaffrey no 3**Results for: **lcl|61181** None(206bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|61181

lcl|61181

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

61183

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**BLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

**Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

## Results Statistics

Effective search space 3582

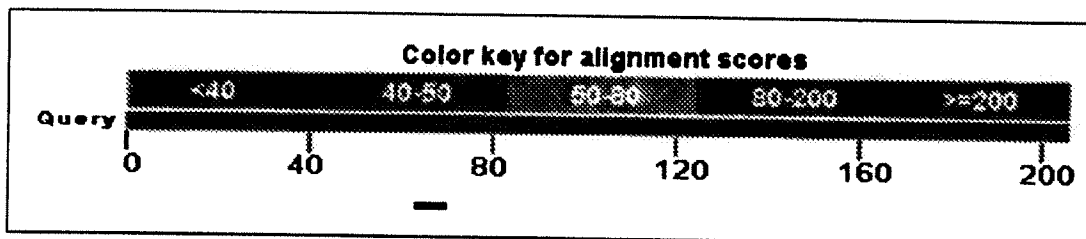
### Graphic Summary

#### Distribution of 1 Blast Hits on the Query Sequence

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#)**Plot of lcl|61181 vs 61183 [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer

**Sequences producing significant alignments:**

(Click headers to sort columns)

61183	13.9	13.9	3%	0.23	100%
-------	------	------	----	------	------

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) 

>lcl|61183  
Length=25

Score = 13.9 bits (14), Expect = 0.23  
Identities = 7/7 (100%), Gaps = 0/7 (0%)  
Strand=Plus/Plus

Query	65	GCCAAGT	71
Sbjct	18	GCCAAGT	24

[Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) 



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Blast 2 sequences

### seq id no:3 vs. McCaffrey no 4

Results for: **lcl|4723 None(206bp)**

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|4723

lcl|4723

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

206

#### Subject ID

4725

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [Taxonomy reports](#)

## Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 3582

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### seq id no:3 vs. McCaffrey no 4

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|4723

lcl|4723

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

4725

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**BLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 3582

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

---

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

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Blast 2 sequences

### seq id no:3 vs. McCaffrey no 5

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|21471

lcl|21471

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

21473

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 3582

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

**[?]**

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### seq id no:3 vs. McCaffrey no 6

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|31433

lcl|31433

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

206

#### Subject ID

31435

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#)

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

## Results Statistics

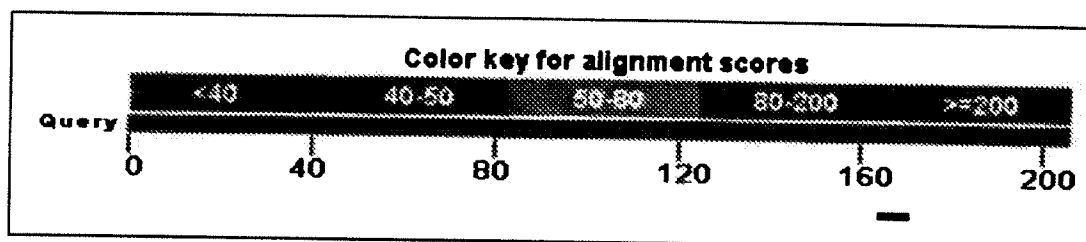
Effective search space 3582

### Graphic Summary

## Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





[Dot Matrix View](#) **Plot of lcl|31433 vs 31435 [?]**

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

**Descriptions**

Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer

**Sequences producing significant alignments:**

(Click headers to sort columns)

31435	13.9	13.9	3%	0.23	100%
-------	------	------	----	------	------

Alignments Select All Get selected sequences Distance tree of results Multiple alignment 

>lcl|31435  
Length=25

Score = 13.9 bits (14), Expect = 0.23  
Identities = 7/7 (100%), Gaps = 0/7 (0%)  
Strand=Plus/Plus

Query	166	GAACTCC	172
Sbjct	11	GAACTCC	17

Select All Get selected sequences Distance tree of results Multiple alignment 

**BLAST Basic Local Alignment Search Tool**

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Blast 2 sequences

**seq id no:3 vs. McCaffrey no 7**Results for: 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|38455

lcl|38455

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

206

**Subject ID**

38457

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**BLASTN 2.2.22+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 3582

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

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Blast 2 sequences

### SEQ ID NO. 10 vs. McCaffrey NO.1

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|45183

lcl|45183

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

71

#### Subject ID

45185

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408148	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**



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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### SEQ ID NO. 10 vs. McCaffrey NO.2

Results for:  

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|53051

lcl|53051

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

53053

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.




**BLAST Basic Local Alignment Search Tool**

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Blast 2 sequences

**SEQ ID NO. 10 vs. McCAFFREY NO.3**

Results for:  

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|3921

lcl|3921

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

3923

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

**Search Parameters**

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

---

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### SEQ ID NO. 10 vs. McCaffrey NO.4

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|59547

lcl|59547

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

71

#### Subject ID

59549

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### SEQ ID NO. 10 vs. McCaffrey NO.5

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|10651

lcl|10651

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

71

#### Subject ID

10653

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### SEQ ID NO. 10 vs. McCaffrey NO.6

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|26449

lcl|26449

#### Description

None

#### Molecule type

nucleic acid

#### Query Length

71

#### Subject ID

26451

#### Description

None

#### Molecule type

nucleic acid

#### Subject Length

25

#### Program

BLASTN 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

## Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



## BLAST Basic Local Alignment Search Tool

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Blast 2 sequences

### SEQ ID NO. 10 vs. McCAFFREY NO.7

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

lcl|32359

lcl|32359

**Description**

None

**Molecule type**

nucleic acid

**Query Length**

71

**Subject ID**

32361

**Description**

None

**Molecule type**

nucleic acid

**Subject Length**

25

**Program**

BLASTN 2.2.22+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

- No significant similarity found. For reasons why, [click here](#)

Other reports: [Search Summary](#) [[Taxonomy reports](#)]

### Search Parameters

Program	blastn
Word size	7
Expect value	10
Hittlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L,m;
Genetic Code	1

### **Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

### **Results Statistics**

Effective search space 1320

[Graphic Summary](#)

### **Distribution of Blast Hits on the Query Sequence**

[?]

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An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.